What is claimed is:

1. A method to selectively produce para-hydroxybenzoic acid in plant stem tissue comprising:

a. growing a plant under suitable conditions, the plant comprising

i. an endogenous source of para-coumaroyl-CoA;

ii. a 4-hydroxycinnamoyl-CoA hydratase/lyase (HCHL) expression cassette comprising a tissue-specific promoter isolated from a cellulose synthase gene encoding a protein involved in the formation of a cellulose synthesis catalytic complex, wherein said cellulose synthesis catalytic complex catalyzes cellulose synthesis in secondary cell wall formation in plant vascular tissue, said tissue-specific promoter operably linked to a nucleic acid molecule encoding a 4-hydroxycinnamoyl-CoA hydratase/lyase enzyme; and

iii. a gene encoding a para-hydroxybenzoic acid UDP-glucosyltransferase;

b. recovering unconjugated para-hydroxybenzoic acid and para-hydroxybenzoic acid glucoside from the plant;

c. hydrolyzing para-hydroxybenzoic acid glucoside; and

d. recovering unconjugated para-hydroxybenzoic acid.

2. The method according to Claim 1 wherein the plant is selected from the group consisting of tobacco, *Arabidopsis,* sugar beet, sugar cane, soybean, rapeseed, sunflower, cotton, corn, alfalfa, wheat, barley, oats, sorghum, rice, canola, millet, beans, peas, rye, flax, and forage grasses.

3. A method according to Claim 1 wherein the tissue-specific promoter is isolated from a gene selected from the group consisting of: *AtCesA4 (IRX5), AtCesA7 (IRX3), AtCesA8 (IRX1), ZmCesA10, ZmCesA11, ZmCesA12,* the *Oryza savita* (japonica cultivar) ortholog of *ZmCesA10*, the *Oryza savita* (japonica cultivar) ortholog of *ZmCesA11*, and the *Oryza savita* (japonica cultivar) ortholog of *ZmCesA12*.

4. A method according to Claim 3 wherein the tissue-specific promoter is selected from the group consisting of SEQ ID Nos:26, 43, 44, 45, 46, 49, 81, 82, and 83.

5. A method according to Claim 1 wherein the HCHL expression cassette is represented by SEQ ID NO:30.

6. A method according to Claim 4 wherein the nucleic acid molecule encoding HCHL is isolated from a bacterium selected from the group consisting of Pseudomonas, Caulobacter, Delftia, Sphingomonas, and Amycolatopsis.

7. A method according to Claim 6 wherein the bacteria is selected from the group consisting of *Pseudomonas putida* (DSM 12585), *Pseudomonas fluorescens* AN103, *Pseudomonas putida* WCS358, *Pseudomonas sp.* HR199, *Delftia acidovorans*, *Amycolatopsis sp.* HR167, *Sphingomonas paucimobilis*, and *Caulobacter crescentus*.

8. A method according to Claim 6 wherein the nucleic acid molecule encoding HCHL is selected from the group consisting of SEQ ID NO:5, 58, 59, 60, 62, 63, and 64.

9. A method according to Claim 6 wherein the nucleic acid molecule encoding HCHL encodes the polypeptide of SEQ ID 61.

10. A method according to Claim 6 wherein the nucleic acid molecule encoding HCHL coding is isolated from *Psuedomonas putida* DSM 12585.

11. A method according to Claim 8 wherein the nucleic acid molecule encoding HCHL encodes the polypeptide of SEQ ID NO:6.

12. A method according to Claim 11 wherein the nucleic acid molecule encoding HCHL is SEQ ID NO:5.

13. A method according to Claim 1 wherein the gene encoding the para-hydroxybenzoic acid UDP-glucosyltransferase is endogenous or exogenous to the plant.

14. A method according to Claim 13 wherein the gene encoding the para-hydroxybenzoic acid UDP-glucosyltransferase is recombinantly expressed in the plant whereby para-hydroxybenzoic acid glucose ester is selectively produced.

15. The method according to Claim 14 wherein the gene encoding the para-hydroxybenzoic acid UDP-glucosyltransferase is selected from the group consisting of SEQ ID NOs:65, 66, and 67.

16. The method according to Claim 1 wherein the tissue-specific promoter of said HCHL expression cassette preferentially expresses active HCHL in said plant stem tissue at levels at least ten times higher than expression levels measured in leaf tissue of said plant.

17. A method to selectively produce para-hydroxybenzoic acid in plant stem tissue comprising:

a. Providing a plant comprising
    i. an endogenous source of para-coumaroyl-CoA;
    ii. a 4-hydroxycinnamoyl-CoA hydratase/lyase (HCHL) expression cassette comprising a tissue-specific promoter

isolated from a cellulose synthase gene encoding a protein involved in the formation of the cellulose synthesis catalytic complex, the tissue-specific promoter operably linked to a nucleic acid molecule encoding a 4-hydroxycinnamoyl-CoA hydratase/lyase enzyme from *Caulobacter crescentus* having at least 50% higher catalytic efficiency in converting para-hydroxycinnamoyl-CoA to para-hydroxybenzoic acid in comparison to catalystic efficienty of an HCHL enzyme from *Psuedomonas putida* or *Pseudomonas fluorescens* expressed under similar conditions; wherein said cellulose synthesis catalytic complex catalyzes cellulose synthesis in secondary cell wall formation in plant vascular tissue; and

iii. a gene encoding a para-hydroxybenzoic acid UDP-glucosyltransferase;

b. growing a plant under suitable conditions whereby unconjugated para-hydroxybenzoic acid and para-hydroxybenzoic acid glucosides are produced;

c. recovering unconjugated para-hydroxybenzoic acid and para-hydroxybenzoic acid glucoside from the plant;

d. hydrolyzing para-hydroxybenzoic acid glucoside; and

e. recovering unconjugated para-hydroxybenzoic acid.

18. A method according to Claim 17 wherein said nucleic acid molecule encodes an amino acid sequence as provided by SEQ ID NO:61.

19. The method according to Claim 17 wherein the plant is selected from the group consisting of tobacco, *Arabidopsis,* sugar beet, sugar cane, soybean, rapeseed, sunflower, cotton, corn, alfalfa, wheat, barley, oats, sorghum, rice, canola, millet, beans, peas, rye, flax, and forage grasses.

20. A method according to Claim 17 wherein the tissue-specific promoter is isolated from a gene selected from the group consisting of: *AtCesA4 (IRX5)*, *AtCesA7 (IRX3), AtCesA8 (IRX1), ZmCesA10*, *ZmCesA11*, *ZmCesA12*, the *Oryza savita* (japonica cultivar) ortholog of *ZmCesA10*, the *Oryza savita* (japonica cultivar) ortholog of *ZmCesA11*, and the *Oryza savita* (japonica cultivar) ortholog of *ZmCesA12*.

21. A method according to Claim 20 wherein the tissue-specific promoter is selected from the group consisting of SEQ ID NOs:26, 43, 44, 45, 46, 49, 81, 82, and 83.

22. A method according to Claim 17 wherein the gene encoding para-hydroxybenzoic acid UDP-glucosyltransferase is endogenous or exogenous to the plant.

23. A method according to Claim 22 wherein the gene encoding para-hydroxybenzoic acid UDP-glucosyltransferase is recombinantly expressed in the plant whereby para-hydroxybenzoic acid glucose ester is selectively produced.

24. The method according to Claim 23 wherein the gene encoding para-hydroxybenzoic acid UDP-glucosyltransferase is selected from the group consisting of SEQ ID NOs:65, 66, and 67.